

Sequence Homology Search

SEQ ID NO: 97

RESULT 1

US-09-946-374-374

; Sequence 374, Application US/09946374

; Publication No. US20030073129A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Botstein, David

; APPLICANT: Desnoyers, Luc

; APPLICANT: Eaton, Dan L.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Fong, Sherman

; APPLICANT: Gao, Wei-Qiang

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, Christopher J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Roy, Margaret Ann

; APPLICANT: Smith, Victoria

; APPLICANT: Stewart, Timothy A.

; APPLICANT: Tumas, Daniel

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

; TITLE OF INVENTION: Acids Encoding the Same

; FILE REFERENCE: P2830P1C1

; CURRENT APPLICATION NUMBER: US/09/946,374

; CURRENT FILING DATE: 2001-09-04

Query Match 100.0%; Score 2323; DB 12; Length 450;
Best Local Similarity 100.0%; Pred. No. 2.5e-210;
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDIFYQVYFLALAADWLQA 60
|
Db 1 MLVTAYLAFVGLLASCLGLELSRCRAKPPGRACSNPSFLRFQLDIFYQVYFLALAADWLQA 60
Qy 61 PYLYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLSLTYSLCCL 120
|
Db 61 PYLYKLYQHYYFLEGQIAILYVCGLASTVLFGLVASSLVDWLGRKNSCVLSLTYSLCCL 120
Qy 121 TKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHV 180
|
Db 121 TKLSQDYFVLLVGRALGGLSTALLFSAFEAWYIHEHVERHDFPAEWIPATFARAAFWNHV 180
Qy 181 LAVVAGVAAEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGL 240
|
Db 181 LAVVAGVAAEAVASWIGLGPVAPFVAAIPLLALAGALALRNWGENYDRQRAFSRTCAGGL 240
Qy 241 RCLLSDRRVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFFSSEMAASLLGSSLYR 300
|
Db 241 RCLLSDRRVLLLGTIQALFESVIFIFVFLWTPVLDPHGAPLGIIFFSSEMAASLLGSSLYR 300
Qy 301 IATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSPGQESPVESFIAFLLIELACGLYFPS 360
|
Db 301 IATSKRYHLQPMHLLSLAVLIVVFSLFMLTFSTSPGQESPVESFIAFLLIELACGLYFPS 360
Qy 361 MSFLRRKVIPETEQAGVLNWFVRPLHSLACLGLLVLDHSDRKTGTRNMFICSAMVMAL 420
|
Db 361 MSFLRRKVIPETEQAGVLNWFVRPLHSLACLGLLVLDHSDRKTGTRNMFICSAMVMAL 420
Qy 421 LAVVGLFTVVRHDAELRVSPTEEPYAPEL 450

Db

|||||
421 LAVVGLFTVVRHDAELRVSPTEEPYAPEL 450